

## SEQUENCE LISTING

<110> Napier, Johnathan A.  
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Zank, Thorsten  
Zahringer, Ulrich

<120> Novel method for the production of polyunsaturated fatty acids

<130> 13478-00001-US

<140> US 10/539,891  
<141> 2005-06-17

<150> PCT/EP2003/014054  
<151> 2003-12-11

<150> GB 0229578.0  
<151> 2002-12-19

<150> GB 0316989.3  
<151> 2003-07-21

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<170> PatentIn version 3.4

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Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln			
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His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp			
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Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys
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gat	gac	cca	atc	aaa	gga	att	gat	gat	gtg	aac	atg	gga	act	ttc	aat
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn
						85				90			95		
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Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu
						100			105			110			
cgt	atg	cga	gtt	cgt	gca	gaa	gga	ctt	atg	gat	gga	tct	cct	ttg	ttc
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe
						115			120			125			
tac	att	aga	aaa	att	ctt	gaa	aca	atc	ttc	aca	att	ctt	ttt	gca	ttc
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe
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Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly
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Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His
						165			170			175			
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Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val
						180			185			190			
gga	aac	ttt	tta	caa	gga	ttc	tca	tct	ggt	ggt	tgg	aaa	gag	cag	cac
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His
						195			200			205			
aat	gtg	cat	cac	gca	aca	aat	gtt	gtt	gga	cga	gac	gga	gat	ctt	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu
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Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr
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tct	cag	gat	tca	tgg	gtt	atg	act	cta	ttc	aga	tgg	caa	cat	gtt	cat
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His
						245			250			255			
tgg	aca	ttc	atg	tta	cca	ttc	ctc	cgt	ctc	tgg	ctt	ctt	cag	tca	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser
						260			265			270			
atc	att	ttt	gtt	agt	cag	atg	cca	act	cat	tat	tat	gac	tat	tac	aga
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg
						265			270			275			

275	280	285	
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp			912
290	295	300	
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met			960
305	310	315	320
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val			1008
325	330	335	
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn			1056
340	345	350	
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met			1104
355	360	365	
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			1152
370	375	380	
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr			1200
385	390	395	400
gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr			1248
405	410	415	
atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe			1296
420	425	430	
cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala			1344
435	440	445	
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<p>Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  20 25 30</p>			
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His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
 100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
 115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
 130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
 145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
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Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val  
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His  
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu  
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr  
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His  
 245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser  
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Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg  
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Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
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Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
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Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
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Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
 340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
 355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
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Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

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ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144  
 Leu Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala  
 35 40 45

gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192  
 Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp  
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65 70 75 80	
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Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys	
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Met Leu Ala Lys Tyr Cys Ile Gly Glu Xaa Val Pro Ser Ala Gly Asp	
100 105 110	
gac aag ttt aag aaa gca act ctg rag tat gca gat gcc gaa aat gaa	384
Asp Lys Phe Lys Lys Ala Thr Leu Xaa Tyr Ala Asp Ala Glu Asn Glu	
115 120 125	
gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt	432
Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser	
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Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly	
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Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu	
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Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val	
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Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg	
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Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln	
260 265 270	
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Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr	
275 280 285	
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca	912

Leu	Ala	Leu	Lys	Ser	Ile	Phe	Leu	Asp	Asp	Phe	Leu	Ala	Tyr	Phe	Thr	
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Asn	Ile	Phe	Phe	Gln	Gly	Lys	Leu	Leu	Tyr	Ala	Phe	Tyr	Met	Phe	Val	
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Gln	Val	Ala	His	Val	Val	Asp	Asp	Val	Ala	Phe	Pro	Thr	Pro	Glu	Gly	
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Asp	Phe	Ser	Pro	Arg	Ser	Trp	Phe	Trp	Gly	His	Val	Ser	Gly	Gly	Leu	
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Tyr	Pro	Ala	Ile	Gln	Pro	Ile	Val	Glu	Lys	Thr	Cys	Lys	Glu	Phe	Asp	
435																
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Val	Pro	Tyr	Val	Ala	Tyr	Pro	Thr	Phe	Trp	Thr	Ala	Leu	Arg	Ala	His	
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 Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly  
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 Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu  
 210 215 220  
  
 Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val  
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 Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg  
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Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln  
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 Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr  
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 Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr  
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 Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe  
 305 310 315 320  
 Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val  
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 Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe  
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 Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu  
 405 410 415  
 Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His  
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 Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp  
 435 440 445  
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Tyr Asp Val Ser Ala Trp Val Asn Phe  
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by Wallis & Browse (ABB 1999)

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Thr Tyr Asp Val Ser Ala Trp Val Asn  
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in GenBank AAD45877

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